GenCore version 4.5

OM protein - protein search, using sw model

Run on: August 28, 2002, 17:25:59 ; Search time 37.53 Seconds
(without alignments)
576.075 Million cell updates/sec

Title: US-09-502-984B-1
Perfect score: 1194
Sequence: 1 APPPNLPDPKFESKAALLAA.....GGFWSAWSEPVSLLTPSDLD 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1194	100.0	508	1	ZUHUR	erythropoietin rec
2	982.5	82.3	507	1	A32385	erythropoietin rec
3	981.5	82.2	507	1	A46713	erythropoietin rec
4	966.5	80.9	265	2	S14081	erythropoietin rec
5	205	17.2	625	2	S35317	hematopoietic grow
6	198	16.6	626	2	S37622	proto-oncogene - m
7	185	15.5	579	2	B45266	MPL-K protein prec
8	185	15.5	635	2	A45266	MPL-P protein prec
9	159	13.3	581	2	I45971	prolactin receptor
10	148	12.4	616	2	A30304	prolactin receptor
11	144.5	12.1	831	2	JQ1655	prolactin receptor
12	136.5	11.4	830	2	I50455	prolactin receptor
13	128	10.7	288	2	B59405	prolactin receptor
14	128	10.7	376	2	A59405	prolactin receptor
15	128	10.7	622	2	A40144	prolactin receptor
16	126	10.6	292	2	I77525	prolactin receptor
17	126	10.6	303	2	I77524	prolactin receptor
18	126	10.6	522	2	B45268	interleukin-9 rece
19	126	10.6	608	2	I53269	prolactin receptor
20	123.5	10.3	677	2	S33608	somatotropin-bindi
21	121.5	10.2	634	2	S33339	somatotropin recep
22	121	10.1	310	2	A29884	prolactin receptor
23	121	10.1	412	2	A41070	prolactin receptor
24	121	10.1	610	2	A34631	lactogen receptor
25	121	10.1	610	2	A36116	prolactin receptor
26	117.5	9.8	638	2	S12136	somatotropin recep
27	117	9.8	608	2	S32823	somatotropin recep
28	116.5	9.8	638	2	B28176	somatotropin recep
29	116	9.7	897	1	A39255	cytokine receptor
30	113	9.5	630	2	I51086	prolactin receptor
31	111.5	9.3	1097	2	S17308	leukemia inhibitor
32	108.5	9.1	279	2	B32985	somatotropin-bindi
33	108.5	9.1	467	2	I56896	gene gfi-2 protein
34	108.5	9.1	638	2	A33505	somatotropin recep
35	108	9.0	976	2	A36355	protein-tyrosine k
36	108	9.0	1825	2	C88400	protein H19M22.1 [
37	108	9.0	1825	2	T32828	hypothetical prote
38	107	9.0	468	2	A45268	interleukin-9 rece
39	106.5	8.9	378	2	A40266	interleukin-3 rece
40	105.5	8.8	975	2	I48974	receptor-protein t
41	104	8.7	2594	2	A35774	kinase-related pro
42	102	8.5	896	1	A35782	cytokine receptor
43	101	8.5	977	2	S49004	tyrosine kinase Mp
44	100.5	8.4	917	2	I49699	glycoprotein 130 -
45	99	8.3	1863	2	S46217	protein-tyrosine-p

ALIGNMENTS

RESULT 1
ZUHUR
erythropoietin receptor precursor - human
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 05-Apr-1995 #text_change 22-Jun-1999
C;Accession: A43799; A60160; A49824; A53958; A55280; I52563
R;Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.
Blood 76, 31-35, 1990
A;Title: Human erythropoietin receptor: cloning, expression, and biologic characteriz
A;Reference number: A43799; MUID:90304340
A;Accession: A43799
A;Molecule type: mRNA
A;Residues: 1-508 <JON>
A;Cross-references: GB:M60459; NID:g182244; PIDN:AAA52403.1; PID:g182245
R;Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.
Blood 76, 24-30, 1990
A;Title: The gene for the human erythropoietin receptor: analysis of the coding seque
A;Reference number: A60160; MUID:90304334
A;Accession: A60160
A;Status: not compared with conceptual translation
A;Molecule type: mRNA; DNA
A;Residues: 1-101,'R',103-188,'RP',191-243,'E',245-508 <WIN>
R;Noguchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D.
Blood 78, 2548-2556, 1991
A;Title: Cloning of the human erythropoietin receptor gene.
A;Reference number: A49824; MUID:92399733
A;Accession: A49824
A;Molecule type: DNA
A;Residues: 1-508 <NOG>
A;Cross-references: GB:S45332; NID:g255496; PIDN:AAB23271.1; PID:g255497
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIN:113293, NCBIP:113294)
R;Ehrenman, K.; St. John, T.
Exp. Hematol. 19, 973-977, 1991
A;Title: The erythropoietin receptor gene: cloning and identification of multiple tra
A;Reference number: A53958; MUID:91372359
A;Accession: A53958
A;Molecule type: mRNA
A;Residues: 1-508 <EHR>
R;Penny, L.A.; Forget, B.G.
Genomics 11, 974-980, 1991
A;Title: Genomic organization of the human erythropoietin receptor gene.
A;Reference number: A55280; MUID:92147143
A;Accession: A55280
A;Molecule type: DNA
A;Residues: 1-17;381-387,'LLEQQQDA',391-395;504-508 <PEN>
A;Note: sequence modified after extraction from NCBI backbone
A;Note: the authors translated the codon GAT for residue 31 as B
A;Note: an insert compared to other published sequences is considered by authors as l
R;Maouche, L.; Tournamille, C.; Hattab, C.; Boffa, G.; Cartron, J.P.; Chretien, S.
Blood 78, 2557-2563, 1991
A;Title: Cloning of the gene encoding the human erythropoietin receptor.

A;Reference number: I52563; MUID:92399734
A;Accession: I52563
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-96 <RES>
A;Cross-references: GB:M76595; NID:g182147; PIDN:AAA52393.1; PID:g553281
C;Genetics:
A;Gene: GDB:EPOR
A;Cross-references: GDB:125242; OMIM:133171
A;Map position: 19p13.3-19p13.2
A;Introns: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
C;Superfamily: erythropoietin receptor; cytokine receptor homology
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-508/Product: erythropoietin receptor #status predicted <MAT>
F;52-250/Domain: extracellular #status predicted <EXT>
F;52-239/Domain: cytokine receptor homology <CRS>
F;233-237/Region: WSXWS motif
F;251-272/Domain: transmembrane #status predicted <TMM>
F;273-508/Domain: intracellular #status predicted <INT>
F;52-62,91-107/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1194; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 8.7e-102;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 APPPNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     25 APPPNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLE 84

Qy     61 DEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAASGAPRYHRVIHINEVVL 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     85 DEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAASGAPRYHRVIHINEVVL 144

Qy    121 LDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGNGAGSVQRVEILEGRTE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    145 LDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGNGAGSVQRVEILEGRTE 204

Qy    181 CVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSDLD 225
          |||||||||||||||||||||||||||||||||||||||||||||
Db    205 CVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSDLD 249
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RESULT 2
A32385
erythropoietin receptor precursor, membrane-bound form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 05-Apr-1995 #text_change 22-Jun-1999
C;Accession: A41686; A32385; S13249
R;Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
Mol. Cell. Biol. 11, 5527-5533, 1991
A;Title: Unregulated expression of the erythropoietin receptor gene caused by insertion
A;Reference number: A41686; MUID:92017832
A;Accession: A41686
A;Molecule type: mRNA
A;Residues: 1-507 <HIN>
A;Cross-references: GB:S59388; NID:g237036; PIDN:AAB20029.1; PID:g237037
A;Experimental source: murine erythroleukemia (MEL) cell line F5-5
R;D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.
Cell 57, 277-285, 1989
A;Title: Expression cloning of the murine erythropoietin receptor.
A;Reference number: A32385; MUID:89195238
A;Accession: A32385
A;Molecule type: mRNA
A;Residues: 1-507 <DAA>
A;Cross-references: GB:J04843; NID:g193090; PIDN:AAA37571.1; PID:g309219
A;Experimental source: murine erythroleukemia (MEL) cells, subclone 745
R;Kuramochi, S.; Ikawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990
A;Title: Characterization of murine erythropoietin receptor genes.
A;Reference number: S13249; MUID:91080149
A;Accession: S13249
A;Molecule type: DNA; mRNA
A;Residues: 1-507 <KUR>
A;Cross-references: EMBL:X53081; NID:g50861; PIDN:CAA37248.1; PID:g50862
A;Experimental source: murine erythroleukemia K-1 cells
C;Genetics:
A;Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3
C;Superfamily: erythropoietin receptor; cytokine receptor homology
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-507/Product: erythropoietin receptor #status predicted <MAT>
F;25-249/Domain: extracellular #status predicted <EXT>
F;52-238/Domain: cytokine receptor homology <CRS>
F;250-271/Domain: transmembrane #status predicted <TMM>
F;272-507/Domain: intracellular #status predicted <INT>
F;52-62,90-106/Disulfide bonds: #status predicted
F;75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.3%; Score 982.5; DB 1; Length 507;
Best Local Similarity 83.1%; Pred. No. 2.3e-82;
Matches 187; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

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Qy      1 APPPNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLE 60
          || |:|||||||||||||:|| |||||||:||||||||||||||:|:   |||||||||
Db     25 APSPSLPDPKFESKAALLASRGSEELLCFTQRLEDLVCFWEEAASSGM-DFNYSFSYQLE 83

Qy     61 DEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAASGAPRYHRVIHINEVVL 120
            |  | | |||||| ||:||||||||||||||||||||:|| |||:|||||:||||||||
Db     84 GESRKSCSLHQAPTVRGSVRFWCSLPTADTSSFVPLELQVTEASGSPRYHRIIHINEVVL 143

Qy    121 LDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGNGAGSVQRVEILEGRTE 180
          |||| ||:|| |:|  ||||||||||  |||:||||||||||||| ||  ||||:||||||
Db    144 LDAPAGLLARRAEEGSHVVLRWLPPPGAPMTTHIRYEVDVSAGNRAGGTQRVEVLEGRTE 203

Qy    181 CVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSDLD 225
          |||||||| ||||||||||||||| |||||||| |||| ||||
Db    204 CVLSNLRGGTRYTFAVRARMAEPSFSGFWSAWSEPASLLTASDLD 248
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RESULT 3
A46713
erythropoietin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A46713
R;Masuda, S.; Nagao, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sasa
J. Biol. Chem. 268, 11208-11216, 1993
A;Title: Functional erythropoietin receptor of the cells with neural characteristics.
A;Reference number: A46713; MUID:93266574
A;Accession: A46713
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-507 <MAS>
A;Cross-references: GB:D13566; NID:g286209; PIDN:BAA02761.1; PID:g286210
A;Experimental source: PC12 and erythroid cells
A;Note: sequence extracted from NCBI backbone (NCBIN:132811, NCBIP:132813)
C;Superfamily: erythropoietin receptor; cytokine receptor homology
C;Keywords: cytokine receptor; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-507/Product: erythropoietin receptor #status predicted <MAT>
F;25-249/Domain: extracellular #status predicted <EXT>
F;52-238/Domain: cytokine receptor homology <CRS>
F;250-271/Domain: transmembrane #status predicted <TMM>
F;272-507/Domain: intracellular #status predicted <INT>
F;75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.2%; Score 981.5; DB 1; Length 507;
Best Local Similarity 82.7%; Pred. No. 2.9e-82;
Matches 186; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

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Qy      1 APPPNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLE 60
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Db      25 ASSPSLPDPKFESKAALLASRGSEELLCFTQRLEDLVCFWEEAANSGMG-FNYSFSYQLE 83

Qy      61 DEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAASGAPRYHRVIHINEVVL 120
           |  | ||||||||  ||::||||||||||||||||||:|| |||:|||||:||||||||
Db      84 GESRKSCRLHQAPTVRGSMRFWCSLPTADTSSFVPLELQVTEASGSPRYHRIIHINEVVL 143

Qy     121 LDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGNGAGSVQRVEILEGRTE 180
           |||| ||:|| |:|  |||||||||  |||:||||||||||||| ||  ||||:||||||
Db     144 LDAPAGLLARRAEEGSHVVLRWLPPPGAPMTTHIRYEVDVSAGNRAGGTQRVEVLEGRTE 203

Qy     181 CVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSDLD 225
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Db     204 CVLSNLRGGTRYTFAVRARMAEPSFSGFWSAWSEPASLLTASDLD 248


RESULT   4
S14081
erythropoietin receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S14081; I49653
R;Kuramochi, S.; Ikawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990
A;Title: Characterization of murine erythropoietin receptor genes.
A;Reference number: S13249; MUID:91080149
A;Accession: S14081
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-265 <KUR>
R;Lacombe, C.; Chretien, S.; Lemarchandel, V.; Mayeux, P.; Romeo, P.
J. Biol. Chem. 266, 6952-6956, 1991
A;Title: Spleen focus-forming virus long terminal repeat insertional activation of the m
A;Reference number: I49653; MUID:91201346
A;Accession: I49653
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-24 <RES>
A;Cross-references: GB:M62360; NID:g193199; PIDN:AAA37582.1; PID:g193200
C;Superfamily: erythropoietin receptor; cytokine receptor homology
C;Keywords: cytokine receptor; transmembrane protein
F;52-238/Domain: cytokine receptor homology <CRS>


  Query Match             80.9%;  Score 966.5;  DB 2;  Length 265;
  Best Local Similarity   82.9%;  Pred. No. 3e-81;
  Matches  184;  Conservative   13;  Mismatches   24;  Indels    1;  Gaps    1;

Qy       1 APPPNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLE 60
           || |:|||||||||||||:|| |||||||:|||||||||||||:|:   |||||||||
Db      25 APSPSLPDPKFESKAALLASRGSEELLCFTQRLEDLVCFWEEAASSGM-DFNYSFSYQLE 83

Qy      61 DEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAASGAPRYHRVIHINEVVL 120
           |  | | |||||| ||:||||||||||||||||||:|| |||:|||||:||||||||
Db      84 GESRKSCSLHQAPTVRGSVRFWCSLPTADTSSFVPLELQVTEASGSPRYHRIIHINEVVL 143

Qy     121 LDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGNGAGSVQRVEILEGRTE 180
           |||| ||:|| |:|  |||||||||  |||:||||||||||||| ||  ||||:||||||
Db     144 LDAPAGLLARRAEEGSHVVLRWLPPPGAPMTTHIRYEVDVSAGNRAGGTQRVEVLEGRTE 203

Qy     181 CVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPS 222
           |||||||| |||||||||||||||| ||||||||| |||| |
Db     204 CVLSNLRGGTRYTFAVRARMAEPSFSGFWSAWSEPASLLTAS 245


RESULT   5
S35317
hematopoietic growth factor receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S35317; S35316
R;Skoda, R.C.; Seldin, D.C.; Chiang, M.K.; Peichel, C.L.; Vogt, T.F.; Leder, P.
EMBO J. 12, 2645-2653, 1993
A;Title: Murine c-mpl: a member of the hematopoietic growth factor receptor superfami
A;Reference number: S35316; MUID:93327753
A;Accession: S35317
A;Molecule type: mRNA
A;Residues: 1-625 <SKO>
A;Cross-references: EMBL:Z22649; NID:g394725; PIDN:CAA80365.1; PID:g394726
A;Accession: S35316
A;Molecule type: DNA
A;Residues: 1-70 <SKW>
A;Cross-references: EMBL:Z22657
C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-625/Product: hematopoietic growth factor receptor #status predicted <MAT>
F;26-482/Domain: extracellular #status predicted <EXT>
F;261-265/Region: WGXWS motif
F;465-469/Region: WSXWS motif
F;483-504/Domain: transmembrane #status predicted <TMM>
F;505-625/Domain: intracellular #status predicted <INT>
F;113,117,178,349/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             17.2%;  Score 205;  DB 2;  Length 625;
  Best Local Similarity   25.9%;  Pred. No. 8.1e-11;
  Matches   66;  Conservative   29;  Mismatches  112;  Indels   48;  Gaps    7;

Qy      13 SKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQA 72
           |:   | | | | | ||::  ||| |||:|  :|    | |   |    |  : | |:
Db      25 SQDVFLLALGTEPLNCFSQTFEDLTCFWDEEEAA--PSGTYQLLYAYRGEKPRACPLYSQ 82

Qy      73 PTARGAVRFWCSLPTAD-TSSFVPLELRVTAAS-GAPRYHRVIHINEVVLLDAPVGLVAR 130
                 |: |  |  |    | || | |   |       ||: :: | |   |  : ||
Db      83 SVPTFGTRYVCQFPAQDEVRLFFPLHLWVKNVSLNQTLIQRVLFVDSVGLPAPPRVIKAR 142

Qy     131 LADESGHVVLRW-LPPPETP--MTSHIRYEVDVSAGNGAGSVQRVEILEGRT-------- 179
              : | : : |  | ||    :   :||    |:   | ||  :::|   |
Db     143 GGSQPGELQIHWEAPAPEISDFLRHELRYGPTDSSNATAPSV--IQLLSTETCCPTLWMP 200

Qy     180 ------------------------------ECVLSNLRGRTRYTFAVRARMAEPSFGGF 208
                                           |::| |:    |   :|::    |  |
Db     201 NPVPVLDQPPCVHPTASQPHGPAPFLTVKGGSCLVSGLQASKSYWLQLRSQPDGVSLRGS 260

Qy     209 WSAWSEPVSLLTPSD 223
           |  || ||::  | |
Db     261 WGPWSFPVTVDLPGD 275


RESULT   6
S37622
proto-oncogene - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S37622
R;Vigon, I.; Florindo, C.; Fichelson, S.; Guenet, J.L.; Mattei, M.G.; Souyri, M.; Cos
Oncogene 8, 2607-2615, 1993
A;Title: Characterization of the murine Mpl proto-oncogene, a member of the hematopoi

A;Reference number: S37622; MUID:93390934
A;Accession: S37622
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-626 <VIG>
A;Cross-references: EMBL:X73677; NID:g404318; PIDN:CAA52031.1; PID:g404319


  Query Match             16.6%;  Score 198;  DB 2;  Length 626;
  Best Local Similarity   24.7%;  Pred. No. 3.6e-10;
  Matches   65;  Conservative   30;  Mismatches  112;  Indels   56;  Gaps    7;

Qy      13 SKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQA 72
           |:   | | | | | ||::  ||| |||:|  :|    | |   |    |  : | |:
Db      18 SQDVFLLALGTEPLNCFSQTFEDLTCFWDEEEAA--PSGTYQLLYAYRGEKPRACPLYSQ 75

Qy      73 PTARGAVRFWCSLPT-ADTSSFVPLELRVTAAS-GAPRYHRVIHINEVVLLDAPVGLVAR 130
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Db     76 SVPTFGTRYVCQFPAQVEVRLFFPLHLWVKNVSLNQTLIQRVLFVDSVGLPAPPRVIKAR 135

Qy    131 LADESGHVVLRW-LPPPETP--MTSHIRYEVDVSAGNGAGSVQRVEILEGRT-------- 179
Db    136 GGSQPGELQIHWEAPAPEISDFLRHELRYGPTDSSNATAPSV--IQLLSTETCCPTLWMP 193

Qy    180 ------------------------------------ECVLSNLRGRTRYTFAVRARM 200
Db    194 NPVPVLDQPPCVHPTASQPHGPVRTSPAGEAPFLTVKGGSCLVSGLQASKSYWLQLRSQP 253

Qy    201 AEPSFGGFWSAWSEPVSLLTPSD 223
Db    254 DGVSLRGSWGPWSFPVTVDLPGD 276


RESULT   7
B45266
MPL-K protein precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C;Accession: B45266
R;Vigon, I.; Mornon, J.P.; Cocault, L.; Mitjavila, M.T.; Tambourin, P.; Gisselbrecht, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992
A;Title: Molecular cloning and characterization of MPL, the human homolog of the v-mpl c
A;Reference number: A45266; MUID:92302297
A;Accession: B45266
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-579 <VIG>
A;Cross-references: GB:M90103; NID:g184262; PIDN:AAA69972.1; PID:g184263


  Query Match             15.5%;  Score 185;  DB 2;  Length 579;
  Best Local Similarity   24.5%;  Pred. No. 5e-09;
  Matches   67;  Conservative   30;  Mismatches  117;  Indels   60;  Gaps    9;

Qy      3 PPNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDE 62
Db     17 PQNL--AQVSSQDVSLLASDSEPLKCFSRTFEDLTCFWDEEEAA--PSGTYQLLYAYPRE 72

Qy     63 PWKLCRLHQAPTARGAVRFWCSLP-TADTSSFVPLELRV-TAASGAPRYHRVIHINEVVL 120
Db     73 KPRACPLSSQSMPHFGTRYVCQFPDQEEVRLFFPLHLWVKNVFLNQTRTQRVLFVDSVGL 132

Qy    121 LDAPVGLVARLADESGHVVLRW-LPPPETPMTSHIRYEV-----DVSAGNGAGSVQRVE- 173
Db    133 PAPPSIIKAMGGSQPGELQISWEEPAPE--ISDFLRYELRYGPRDPKNSTGPTVIQLIAT 190

Qy    174 -------------------------------------------ILEGRTECVLSNLRGR 189
Db    191 ETCCPALQRPHSASALDQSPCAQPTMPWQDGPKQTSPSREASALTAEGGS-CLISGLQPG 249

Qy    190 TRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSD 223
Db    250 NSYWLQLRSEPDGISLGGSWGSWSLPVTVDLPGD 283


RESULT   8
A45266
MPL-P protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C;Accession: A45266
R;Vigon, I.; Mornon, J.P.; Cocault, L.; Mitjavila, M.T.; Tambourin, P.; Gisselbrecht, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992
A;Title: Molecular cloning and characterization of MPL, the human homolog of the v-mpl c
A;Reference number: A45266; MUID:92302297
A;Accession: A45266
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-635 <VIG>
A;Cross-references: GB:M90102; NID:g184260; PIDN:AAA69971.1; PID:g184261
C;Keywords: transmembrane protein


  Query Match             15.5%;  Score 185;  DB 2;  Length 635;
  Best Local Similarity   24.5%;  Pred. No. 5.7e-09;
  Matches   67;  Conservative   30;  Mismatches  117;  Indels   60;  Gaps    9;

Qy      3 PPNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDE 62
Db     17 PQNL--AQVSSQDVSLLASDSEPLKCFSRTFEDLTCFWDEEEAA--PSGTYQLLYAYPRE 72

Qy     63 PWKLCRLHQAPTARGAVRFWCSLP-TADTSSFVPLELRV-TAASGAPRYHRVIHINEVVL 120
Db     73 KPRACPLSSQSMPHFGTRYVCQFPDQEEVRLFFPLHLWVKNVFLNQTRTQRVLFVDSVGL 132

Qy    121 LDAPVGLVARLADESGHVVLRW-LPPPETPMTSHIRYEV-----DVSAGNGAGSVQRVE- 173
Db    133 PAPPSIIKAMGGSQPGELQISWEEPAPE--ISDFLRYELRYGPRDPKNSTGPTVIQLIAT 190

Qy    174 -------------------------------------------ILEGRTECVLSNLRGR 189
Db    191 ETCCPALQRPHSASALDQSPCAQPTMPWQDGPKQTSPSREASALTAEGGS-CLISGLQPG 249

Qy    190 TRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSD 223
Db    250 NSYWLQLRSEPDGISLGGSWGSWSLPVTVDLPGD 283


RESULT   9
I45971
prolactin receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C;Accession: I45971
R;Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A;Title: Molecular cloning of the bovine prolactin receptor and distribution of prola
A;Reference number: I45971; MUID:93246019
A;Accession: I45971
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-581 <SCO>
A;Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C;Genetics:
A;Gene: PRLR
C;Superfamily: cytokine receptor homology
F;36-221/Domain: cytokine receptor homology <CRS>


  Query Match             13.3%;  Score 159;  DB 2;  Length 581;
  Best Local Similarity   24.6%;  Pred. No. 1.2e-06;
  Matches   55;  Conservative   36;  Mismatches  103;  Indels   30;  Gaps   10;

Qy     16 ALLAARGPEE----LLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQ 71
Db     20 SLLNGQSPPEKPKLVKCRSPGKETFTCWWEPGADGGL-PTNYTLTYHKEGE----TLIHE 74

Qy     72 APTARGAVRFWCSLPTADTSSFVPLELRVTA------ASGAPRYHRVIHINEVVLLDAPV 125
Db     75 CPDYKTGGPNSCYFSKKHTSIWKMYVITVNAINQMGISSSDPLY---VHVTYIVEPEPPA 131

Qy    126 GLVARL---ADESGHVVLRWLPPPETPMTSH---IRYEVDVSAGNGAGSVQRVEILEGRT 179
Db    132 NLTLELKHPEDRKPYLWIKWSPPTMTDVKSGWFIIQYEIRLKPEKATDWETHFTLKQ--T 189

Qy    180 ECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSD 223
Db    190 QLKIFNLYPGQKYLVQIRCK---PDH-GYWSEWSPESSIQIPND 229


RESULT  10
A30304
prolactin receptor 2 precursor - rabbit
```

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N;Alternate names: prolactin receptor, mammary gland
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Jul-2000
C;Accession: A30304; A60380
R;Edery, M.; Jolicoeur, C.; Levi-Meyrueis, C.; Dusanter-Fourt, I.; Petridou, B.; Boutin,
Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
A;Title: Identification and sequence analysis of a second form of prolactin receptor by
A;Reference number: A30304; MUID:89184578
A;Accession: A30304
A;Molecule type: mRNA
A;Residues: 1-616 <EDE>
A;Cross-references: GB:J04510; NID:g165669; PIDN:AAA31457.1; PID:g165670
R;Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
Int. J. Biochem. 22, 1089-1095, 1990
A;Title: Purification and partial sequence of the rabbit mammary gland prolactin recepto
A;Reference number: A60380; MUID:91146782
A;Accession: A60380
A;Molecule type: protein
A;Residues: 41-58,'X',60-66;90-93,'X',95-96,'X',98-103,'X',105,'NX',108;150-164,'XX',167
A;Note: the amino end of the mature protein was blocked
C;Superfamily: cytokine receptor homology
C;Keywords: blocked amino end; glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-616/Product: prolactin receptor 2 #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
F;235-258/Domain: transmembrane #status predicted <TMM>
F;59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             12.4%;  Score 148;  DB 2;  Length 616;
  Best Local Similarity   24.5%;  Pred. No. 1.4e-05;
  Matches   57;  Conservative   31;  Mismatches  103;  Indels   42;  Gaps   11;

Qy       3 PPNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDE 62
            ||  |          :   | ||:         |   |:|   |  |: | ||: :|  | |
Db      27 PPGKP--------FIFKCRSPEK--------ETFTCWWRPGADGGL-PTNYTLTYHKEGE 69

Qy      63 PWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAAS------GAPRYHRVIHIN 116
                 |: |  :       |      || :    : | | :         |||    : :
Db      70 ----TITHECPDYKTGGPNSCYFSKKHTSIWTIYIITVNATNQMGSSVSDPRY---VDVT 122

Qy     117 EVVLLDAPVGL---VARLADESGHVVLRWLPPPETPMTS---HIRYEVDVSAGNGAGSVQ 170
             :|  | || |   |    |   :: ::||||    : |    ::||: :      |
Db     123 YIVEPDPPVNLTLEVKHPEDRKPYLWVKWLPPTLVDVRSGWLTLQYEIRLKPEKAA--EW 180

Qy     171 RVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSD 223
                :|:  : :|    :|   || :   |   ||||| ||   |:  |:|
Db     181 ETHFAGQQTQFKILSLYPGQKYLVQVRCK---PDH-GFWSVWSPESSIQIPND 229


RESULT  11
JQ1655
prolactin receptor precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C;Accession: JQ1655
R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA se
A;Reference number: JQ1655; MUID:93075121
A;Accession: JQ1655
A;Molecule type: mRNA
A;Residues: 1-831 <TAN>
A;Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A;Experimental source: kidney
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <MAT>
F;36-219/Domain: cytokine receptor homology <CRS1>
F;239-425/Domain: cytokine receptor homology <CRS2>
F;439-462/Domain: transmembrane #status predicted <TMM>
F;59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (covale


  Query Match             12.1%;  Score 144.5;  DB 2;  Length 831;
  Best Local Similarity   23.5%;  Pred. No. 4.2e-05;
  Matches   55;  Conservative   33;  Mismatches  103;  Indels   43;  Gaps   11;

Qy       3 PPNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDE 62
            ||  |          ::  | ||:         |   |:|:      |  | ||:  |  | |
Db     230 PPEKP--------TIIKCRSPEK--------ETFTCWWKPGLDGG-HPTNYTLLYSKEGE 272

Qy      63 PWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAA------SGAPRYHRVIHIN 116
                ::::  |  | |     |      || :    : | |       |  | |   : :
Db     273 E----QVYECPDYRTAGPNSCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHY---VDVT 325

Qy     117 EVVLLDAPVGLVARL---ADESGHVVLRWLPPPETPMTS---HIRYEVDVSAGNGAGSVQ 170
              :|  | || :   |    :   ::|| | |||   : |    : ||: :    |    :
Db     326 YIVQPDPPVNVTLELKKPINRKPYLVLTWSPPPLADVRSGWLTLEYELRLKPEEGE---E 382

Qy     171 RVEILEG-RTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSD 223
               |  | :|:  : :|    :|   :  :   |   | || ||    :  |:|
Db     383 WETIFVGQQTQYKMFSLNPGKKYIIQIHCK---PDHHGSWSEWSSENYIQIPND 433


RESULT  12
I50455
prolactin receptor - pigeon
C;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
C;Accession: I50455
R;Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A;Title: Cloning, expression, and mutational analysis of the pigeon prolactin recepto
A;Reference number: I50455; MUID:94283267
A;Accession: I50455
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-830 <CHE>
A;Cross-references: EMBL:U07694; NID:g466381; PIDN:AAA20646.1; PID:g466382
C;Superfamily: cytokine receptor homology
F;36-220/Domain: cytokine receptor homology <CRS1>
F;240-426/Domain: cytokine receptor homology <CRS2>


  Query Match             11.4%;  Score 136.5;  DB 2;  Length 830;
  Best Local Similarity   23.2%;  Pred. No. 0.00023;
  Matches   55;  Conservative   33;  Mismatches  104;  Indels   45;  Gaps   11;

Qy       4 PNLPDPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEP 63
            ||   |    |  ::  | ||:         |   |:|:  :  |  | ||:  |  | |
Db     226 PNGESP--PEKPTIIKCRSPEK--------ETFTCWWKPGSDGG-HPTNYTLLYSKEGEE 274

Qy      64 WKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAAS------GAPRYHRVIHINE 117
               |::: |  : |    |      || :    : | | :         | |   : :
Db     275 ----RVYECPDYKTAGPNSCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLY---VDVTY 327

Qy     118 VVLLDAPVGLVARL---ADESGHVVLRWLPPPETPMTS---HIRYEVDVSAGNGAGSVQR 171
             :|  | || :   |    :   ::|| | |||   : |    : ||: :          :
Db     328 IVQTDPPVNVTLELKKTVNRKPYLVLTWSPPPLADVRSGWLTLDYELRLKP-------EE 380

Qy     172 VEILE-----GRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSAWSEPVSLLTPSD 223
              |  |      :|   : :|    :|   :  :   |   | || ||    |  |:|
Db     381 AEEWETIFVGQQTHYKMFSLNPGKKYIVQIHCK---PDHHGSWSEWSLEKYLQIPTD 434


RESULT  13
B59405
prolactin receptor short form S1b precursor, breast cancer cells T-47D - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: B59405
R;Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A;Title: Isolation and characterization of two novel forms of the human prolactin rec
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A;Reference number: A59405; MUID:21538812; PMID:11518703
A;Accession: B59405
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-288 <HUZ>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
C;Genetics:
A;Gene: GDB:PRLR
A;Cross-references: GDB:120315; OMIM:176761
A;Map position: 5p13.3-5p13.1
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-288/Product: prolactin receptor, short form S1b #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             10.7%;  Score 128;  DB 2;  Length 288;
  Best Local Similarity   23.8%;  Pred. No. 0.00035;
  Matches   50;  Conservative   33;  Mismatches  107;  Indels   20;  Gaps    9;

Qy      23 PEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFW 82
           ||   | :   |   |:|      |: | ||| :|  | |      :|: |
Db      31 PEIFKCRSPNKETFTCWWRPGTDGGL-PTNYSLTYHREGE----TLMHECPDYITGGPNS 85

Qy      83 CSLPTADTSSFVPLELRVTAAS--GAPRYHRV-IHINEVVLLDAPVGL---VARLADESG 136
           |      || :    : | | :  |:     : : :  :|  | |:      :|  :
Db      86 CHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLELAVEVKQPEDRKP 145

Qy     137 HVVLRWLPPPETPMTS---HIRYEVDVSAGNGAGSVQRVEILEGRTECVLSNLRGRTRYT 193
           :: ::| ||    : :    : ||: :     |     :    :||  : :|    :|
Db     146 YLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAA--EWEIHFAGQQTEFKILSLHPGQKYL 203

Qy     194 FAVRARMAEPSFGGFWSAWSEPVSLLTPSD 223
             || :   |   |:|||||    :  |||
Db     204 VQVRCK---PDH-GYWSAWSPATFIQIPSD 229


RESULT  14
A59405
prolactin receptor short form S1a precursor, breast cancer cells T-47D - human
C;Species: Homo sapiens
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: A59405
R;Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A;Title: Isolation and characterization of two novel forms of the human prolactin recept
A;Reference number: A59405; MUID:21538812; PMID:11518703
A;Accession: A59405
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <HUZ>
A;Cross-references: GB:AF214012; PIDN:AF214012.1
C;Genetics:
A;Gene: GDB:PRLR
A;Cross-references: GDB:120315; OMIM:176761
A;Map position: 5p13.3-5p13.1
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-376/Product: prolactin receptor, short form S1a #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             10.7%;  Score 128;  DB 2;  Length 376;
  Best Local Similarity   23.8%;  Pred. No. 0.0005;
  Matches   50;  Conservative   33;  Mismatches  107;  Indels   20;  Gaps    9;

Qy      23 PEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFW 82
           ||   | :   |   |:|      |: | ||| :|  | |      :|: |
Db      31 PEIFKCRSPNKETFTCWWRPGTDGGL-PTNYSLTYHREGE----TLMHECPDYITGGPNS 85

Qy      83 CSLPTADTSSFVPLELRVTAAS--GAPRYHRV-IHINEVVLLDAPVGL---VARLADESG 136
           |      || :    : | | :  |:     : : :  :|  | |:      :|  :
Db      86 CHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLELAVEVKQPEDRKP 145

Qy     137 HVVLRWLPPPETPMTS---HIRYEVDVSAGNGAGSVQRVEILEGRTECVLSNLRGRTRYT 193
           :: ::| ||    : :    : ||: :     |     :    :||  : :|    :|
Db     146 YLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAA--EWEIHFAGQQTEFKILSLHPGQKYL 203

Qy     194 FAVRARMAEPSFGGFWSAWSEPVSLLTPSD 223
             || :   |   |:|||||    :  |||
Db     204 VQVRCK---PDH-GYWSAWSPATFIQIPSD 229


RESULT  15
A40144
prolactin receptor long form precursor, hepatoma and breast cancer cells - human
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 01-Dec-2000
C;Accession: A40144; A57018
R;Boutin, J.M.; Edery, M.; Shirota, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, D
Mol. Endocrinol. 3, 1455-1461, 1989
A;Title: Identification of a cDNA encoding a long form of prolactin receptor in human
A;Reference number: A40144; MUID:90114212
A;Accession: A40144
A;Molecule type: mRNA
A;Residues: 1-622 <BOU>
A;Cross-references: GB:M31661; NID:g190361; PIDN:AAA60174.1; PID:g190362
R;Fuh, G.; Wells, J.A.
J. Biol. Chem. 270, 13133-13137, 1995
A;Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell
A;Reference number: A57018; MUID:95286597
A;Accession: A57018
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 25-228,'AW' <RES>
A;Cross-references: GB:S78505; NID:g999114; PIDN:AAB34470.1; PID:g999115
C;Genetics:
A;Gene: GDB:PRLR
A;Cross-references: GDB:120315; OMIM:176761
A;Map position: 5p13.3-5p13.1
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-622/Product: prolactin receptor, long form #status predicted <MAT>
F;36-221/Domain: cytokine receptor homology <CRS>
F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             10.7%;  Score 128;  DB 2;  Length 622;
  Best Local Similarity   23.8%;  Pred. No. 0.00095;
  Matches   50;  Conservative   33;  Mismatches  107;  Indels   20;  Gaps    9;

Qy      23 PEELLCFTERLEDLVCFWEEAASAGVGPGNYSFSYQLEDEPWKLCRLHQAPTARGAVRFW 82
           ||   | :   |   |:|      |: | ||| :|  | |      :|: |
Db      31 PEIFKCRSPNKETFTCWWRPGTDGGL-PTNYSLTYHREGE----TLMHECPDYITGGPNS 85

Qy      83 CSLPTADTSSFVPLELRVTAAS--GAPRYHRV-IHINEVVLLDAPVGL---VARLADESG 136
           |      || :    : | | :  |:     : : :  :|  | |:      :|  :
Db      86 CHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYIVQPDPPLELAVEVKQPEDRKP 145

Qy     137 HVVLRWLPPPETPMTS---HIRYEVDVSAGNGAGSVQRVEILEGRTECVLSNLRGRTRYT 193
           :: ::| ||    : :    : ||: :     |     :    :||  : :|    :|
Db     146 YLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAA--EWEIHFAGQQTEFKILSLHPGQKYL 203

Qy     194 FAVRARMAEPSFGGFWSAWSEPVSLLTPSD 223
             || :   |   |:|||||    :  |||
Db     204 VQVRCK---PDH-GYWSAWSPATFIQIPSD 229


Search completed: August 28, 2002, 17:32:26
Job time: 387 sec
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